

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/559,647
Source: IFWP
Date Processed by STIC: 12/16/05

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,647

TIME: 15:39:57

Input Set : A:\ISPH0595USASEQ.txt

Output Set: N:\CRF4\12162005\J559647.raw

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3 <110> APPLICANT: Isis Pharmaceuticals Inc.
4     Rosanne M. Crooke
5     Mark J. Graham
7 <120> TITLE OF INVENTION: MODULATION OF APOLIPOPROTEIN(A) EXPRESSION
9 <130> FILE REFERENCE: ISPH-0595WO2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/559,647
C--> 11 <141> CURRENT FILING DATE: 2005-12-02
11 <150> PRIOR APPLICATION NUMBER: 09/923,515
12 <151> PRIOR FILING DATE: 2001-08-07
14 <150> PRIOR APPLICATION NUMBER: 60/475,402
15 <151> PRIOR FILING DATE: 2003-06-02
17 <160> NUMBER OF SEQ ID NOS: 100
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 20
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Antisense Oligonucleotide
27 <400> SEQUENCE: 1
28 tccgtcatcg ctctcaggg                                20
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 20
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Antisense Oligonucleotide
39 <400> SEQUENCE: 2
40 gtgcgcgcga gcccgaaatc                                20
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 20
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Antisense Oligonucleotide
51 <400> SEQUENCE: 3
52 atgcattctg cccccaagga                                20
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 13938
57 <212> TYPE: DNA
58 <213> ORGANISM: H. sapiens
60 <220> FEATURE:
61 <221> NAME/KEY: CDS
62 <222> LOCATION: (46)...(13692)

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64 <400> SEQUENCE: 4

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65 ctgggattgg gacacacttt ctggacactg ctggccagtc ccaaa atg gaa cat aag      57
66                                     Met Glu His Lys
67                                     1
69 gaa gtg gtt ctt cta ctt ctt tta ttt ctg aaa tca gca gca cct gag      105
70 Glu Val Val Leu Leu Leu Leu Leu Phe Leu Lys Ser Ala Ala Pro Glu
71   5          10          15          20
73 caa agc cat gtg gtc cag gat tgc tac cat ggt gat gga cag agt tat      153
74 Gln Ser His Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr
75          25          30          35
77 cga ggc acg tac tcc acc act gtc aca gga agg acc tgc caa gct tgg      201
78 Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ala Trp
79          40          45          50
81 tca tct atg aca cca cat caa cat aat agg acc aca gaa aac tac cca      249
82 Ser Ser Met Thr Pro His Gln His Asn Arg Thr Thr Glu Asn Tyr Pro
83          55          60          65
85 aat gct ggc ttg atc atg aac tac tgc agg aat cca gat gct gtg gca      297
86 Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala
87          70          75          80
89 gct cct tat tgt tat acg agg gat ccc ggt gtc agg tgg gag tac tgc      345
90 Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys
91          85          90          95          100
93 aac ctg acg caa tgc tca gac gca gaa ggg act gcc gtc gcg cct ccg      393
94 Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro
95          105          110          115
97 act gtt acc ccg gtt cca agc cta gag gct cct tcc gaa caa gca ccg      441
98 Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro
99          120          125          130
101 act gag caa agg cct ggg gtg cag gag tgc tac cat ggt aat gga cag      489
102 Thr Glu Gln Arg Pro Gly Val Gln Glu Cys Tyr His Gly Asn Gly Gln
103          135          140          145
105 agt tat cga ggc aca tac tcc acc act gtc aca gga aga acc tgc caa      537
106 Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln
107          150          155          160
109 gct tgg tca tct atg aca cca cac tcg cat agt cgg acc cca gaa tac      585
110 Ala Trp Ser Ser Met Thr Pro His Ser His Ser Arg Thr Pro Glu Tyr
111          165          170          175          180
113 tac cca aat gct ggc ttg atc atg aac tac tgc agg aat cca gat gct      633
114 Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala
115          185          190          195
117 gtg gca gct cct tat tgt tat acg agg gat ccc ggt gtc agg tgg gag      681
118 Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu
119          200          205          210
121 tac tgc aac ctg acg caa tgc tca gac gca gaa ggg act gcc gtc gcg      729
122 Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala
123          215          220          225
125 cct ccg act gtt acc ccg gtt cca agc cta gag gct cct tcc gaa caa      777
126 Pro Pro Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln
127          230          235          240

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129	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	tac	cat	ggt	aat	825
130	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	
131	245				250					255						260	
133	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	873
134	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	
135				265					270						275		
137	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	921
138	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	
139			280						285					290			
141	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	969
142	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	
143			295					300					305				
145	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	1017
146	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	
147		310					315					320					
149	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	1065
150	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	
151	325				330					335						340	
153	gtc	gcg	cct	ccg	act	ggt	acc	ccg	ggt	cca	agc	cta	gag	gct	cct	tcc	1113
154	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	
155				345					350						355		
157	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	tac	cat	1161
158	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	
159			360						365					370			
161	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	1209
162	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	
163			375					380					385				
165	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	1257
166	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	
167		390					395					400					
169	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	1305
170	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	
171	405				410					415					420		
173	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	1353
174	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	
175				425					430						435		
177	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	1401
178	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	
179			440						445					450			
181	act	gcc	gtc	gcg	cct	ccg	act	ggt	acc	ccg	ggt	cca	agc	cta	gag	gct	1449
182	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	
183			455					460						465			
185	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	1497
186	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	
187		470					475					480					
189	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	1545
190	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	
191	485					490					495					500	
193	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	1593

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194	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	
195					505					510					515		
197	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	1641
198	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	
199					520					525					530		
201	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	1689
202	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	
203					535					540					545		
205	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	1737
206	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	
207					550					555					560		
209	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	agc	cta	1785
210	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	
211	565					570					575					580	
213	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	1833
214	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	
215					585						590				595		
217	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	1881
218	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	
219					600					605					610		
221	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	1929
222	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	
223					615					620					625		
225	tgc	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	1977
226	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	
227					630					635					640		
229	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	2025
230	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	
231	645					650					655					660	
233	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	2073
234	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	
235					665						670				675		
237	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	2121
238	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	
239					680					685					690		
241	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	2169
242	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	
243					695				700					705			
245	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	2217
246	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	
247					710				715					720			
249	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	2265
250	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	
251	725					730					735				740		
253	cca	cac	tgc	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	2313
254	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	
255					745					750					755		
257	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	2361
258	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	

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259		760		765		770		
261	tat	acg	agg	gat	ccc	ggt	gtc	agg
262	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg
263								
265	tgc	tca	gac	gca	gaa	ggg	act	gcc
266	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala
267								
269	ggt	cca	agc	cta	gag	gct	cct	tcc
270	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser
271	805							
273	cct	ggg	gtg	cag	gag	tgc	tac	cat
274	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His
275								
277	aca	tac	tcc	acc	act	gtc	aca	gga
278	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly
279								
281	atg	aca	cca	cac	tcg	cat	agt	cgg
282	Met	Thr	Pro	His	Ser	His	Ser	Arg
283								
285	ggc	ttg	atc	atg	aac	tac	tgc	agg
286	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg
287								
289	tat	tgt	tat	acg	agg	gat	ccc	ggt
290	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly
291	885							
293	acg	caa	tgc	tca	gac	gca	gaa	ggg
294	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly
295								
297	acc	ccg	ggt	cca	agc	cta	gag	gct
298	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala
299								
301	caa	agg	cct	ggg	gtg	cag	gag	tgc
302	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys
303								
305	cga	ggc	aca	tac	tcc	acc	act	gtc
306	Arg	Gly	Thr	Tyr	Ser	Thr	Val	Thr
307								
309	tca	tct	atg	aca	cca	cac	tcg	cat
310	Ser	Ser	Met	Thr	Pro	His	Ser	His
311	965							
313	aat	gct	ggc	ttg	atc	atg	aac	tac
314	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr
315								
317	gct	cct	tat	tgt	tat	acg	agg	gat
318	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp
319								
321	aac	ctg	acg	caa	tgc	tca	gac	gca
322	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala
323								

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4